

Genomic analysis of the principal members of antioxidant enzymes in simulated stresses response and postharvest physiological deterioration in cassava

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Abstract

ROS act as an signaling molecule in the biological growth and development process. The homeostasis of ROS must be kept by different antioxidant defense mechanisms. Currently, superoxide dismutase (SOD), catalase (CAT), and ascorbate peroxidase (APX) as major antioxidant enzymes are not well understood in cassava (*Manihot esculenta*). In this research, 7 SODs, 6 CATs, and 6 APXs were identified from the cassava genome by hidden Markov models, which was supported by gene structure, protein motifs, and phylogenetic relationship analyses. *SOD*, *CAT*, and *APX* genes expressed differentially in different tissues of cassava, of which most *SODs* showed high expression levels. The comprehensive expression profiles revealed the participation of *SOD*, *CAT*, *APX* genes during postharvest physiological deterioration (PPD) of storage root and in response to osmotic stress and ABA as well as *Xanthomonas axonopodis* infection. Together, this study increases our understanding of cassava *SOD*, *CAT*, *APX* genes feature and their potential function during PPD process and in response to biotic and abiotic stresses in cassava, laying a solid foundation for further gene function analysis in cassava.